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1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: MEDICAL RESEARCH COUNCIL
- (B) STREET: 20 PARK CRESCENT
- (C) CITY: LONDON
- (E) COUNTRY: UK
- (F) POSTAL CODE (ZIP): W1N 4AL

(ii) TITLE OF INVENTION: GENE

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5..604

TGTC ATG TTG CGG GCT TTG AAC CGC CTG GCC GCG CGG CCC GGG GGC CAG  
49

CCC CCA ACC CTG CTC CTT CTG CCC GTG CGC GGC CGC AAG ACC CGC CAC  
97

GAT CCG CCT GCC AAG TCC AAG GTC GGG CGC GTG AAA ATG CCT CCT GCA  
145

GTG GAC CCT GCG GAA TTG TTC GTG TTG ACC GAG CGC TAC CGA CAG TAC  
193

CGG GAG ACG GTG CGC GCT CTC AGG CGA GAG TTC ACA TTG GAG GTG CGA  
241

GGG AAA TTG CAC GAG GCC CGA GCC GGG GTT CTG GCT GAG CGC AAG GCG  
289

CAA GAG GCC ATC AGA GAG CAC CAG GAG CTG ATG GCC TGG AAC CGG GAG  
337

GAG AAC CGG AGA CTG CAG GAA CTA CGG ATA GCT AGG TTG CAG CTC GAA  
385

GCA CAG GCC CAG GAG CTG CGG CAG GCT GAG GTC CAG GCC CAG AGG GCC

433

Ala Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala  
130 135 140

CAG GAG GAG CAG GCT TGG GTG CAA CTG AAA GAA CAA GAA GTT CTC AAA  
481

Gln Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys  
145 150 155

CTG CAG GAG GAG GCC AAA AAC TTC ATC ACT CGG GAG AAC CTG GAG GCA  
529

Leu Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala  
160 165 170 175

CGG ATA GAA GAG GCC TTG GAC TCT CCG AAG AGT TAT AAC TGG GCG GTC  
577

Arg Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val  
180 185 190

ACC AAA GAA GGG CAG GTG GTC AGG AAC TGAGAACAGA GGCCTCTCAG  
624

Thr Lys Glu Gly Gln Val Val Arg Asn  
195 200

GCCCAAATAA GGACAGTGCT TGCCTAGGGA CTGGATATTG GGGTAGAAAT  
TGGTGCATCC 684

CAGGAGGGTG GCACAGCCTT GTCCAGAGCA GCCCCCATTC ATTCTAGATT  
TGGCACCAGG 744

TATAGTACCT GTTCTGACAC CACATACAAA CTCCGGACAG CATTAAACTC  
TGGGAAGTTC 804

CTATCACACA GAAGATCAGA CTGGACTGTC CCCTCTAGAA GCCAAGAGCT  
GTCTCCTGAG 864

TTTCTTGGA TAGTGTGAGC CCAATGTTTC CTGCTTTTAT AAATAAACTA  
TTGGAAAGCA 924

(2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro

1 5 10 15

Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp

20 25 30

Pro Pro Ala Lys Ser Lys Val Gly Arg Val Lys Met Pro Pro Ala Val

35 40 45

Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr Arg

50 55 60

Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg Gly

65 70 75 80

Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln

85 90 95

Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu Glu

100 105 110

Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala

115 120 125

Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala Gln

130 135 140

Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys Leu

145 150 155 160

Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg

165 170 175

Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val Thr

180 185 190

(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 998 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION:1..615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CTA CGC GCG CTG AGC CGC CTG GGC GCG GGG ACC CCG TGC AGG CCC  
48

Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro  
205 210 215

CGG GCC CCT CTG GTG CTG CCA GCG CGC GGC CGC AAG ACC CGC CAC GAC  
96

Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp  
220 225 230

CCG CTG GCC AAA TCC AAG ATC GAG CGA GTG AAC ATG CCG CCC GCG GTG  
144

Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val  
235 240 245

GAC CCT GCG GAG TTC TTC GTG CTG ATG GAG CGT TAC CAG CAC TAC CGC  
192

[illegible]

Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr  
380 385 390

AGA GAG GGG CTG GTG GTC AGG CCA CAA CGC AGG GAC TCC TAGGGGCCCA  
625

Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser  
395 400 405

GTAAGGACAG TGCCCGCCAG GGACCATGTA TGTATCATGG CGGAAGAGTT  
GGCCCTGACC 685

TGGAATAAAG CAGTTGGTGT TGCTTATGAG GAAGGTTTCAG CCTTATCCAG  
CACAGCCTTC 745

ACGTTTTGCC CTCTGCTGTC ACCACTTGGT CAGAACTTC CAAACGCAGT  
GCCCTGTTCT 805

GCCGGTGTGT AAAGCCTCAG CGCACCAGGA GACCCTAGAG TGGTTTCCAT  
CTCACAGAGA 865

ATCAGACAGG CCACAGCCCC CTCAGGCAGC CAGGTCATCT GAGTATCATT  
AAGAGTAGTG 925

ATGGGAAGAT TACAGTCTGA GGGCCAAACG TGCCTGCTTC CTGTTTTTGT  
AAATAAAGTT 985

TTGTTGGAAC ACA 998

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro  
1 5 10 15

Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp  
20 25 30

Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val

CCGTCCTGCTTC

35            40            45  
 Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg  
 50            55            60  
 Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg  
 65            70            75            80  
 Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu  
 85            90            95  
 Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu  
 100            105            110  
 Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu  
 115            120            125  
 Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu  
 130            135            140  
 Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu  
 145            150            155            160  
 Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg  
 165            170            175  
 Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr  
 180            185            190  
 Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser  
 195            200            205

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO



(ix) FEATURE:

(B) LOCATION:5..604

TGTC ATG TTG CGC GCT CTG AAC CGC CTG GCG CAG CGG CCG GGA GAC CGG  
49

Met Leu Arg Ala Leu Asn Arg Leu Ala Gln Arg Pro Gly Asp Arg  
210 215 220

CCC CCG ACC CCG CTG CTC CTG CCC GTG CGC GGC CGC AAG ACC CGC CAT  
97

Pro Pro Thr Pro Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His  
225 230 235

GAC CCG CCT GCC AAA TCC AAG GTC GGA CGG GTG CAG ACG CCT CCC GCC  
145

Asp Pro Pro Ala Lys Ser Lys Val Gly Arg Val Gln Thr Pro Pro Ala  
240 245 250

GTG GAC CCT GCG GAA TTC TTC GTG TTG ACC GAG CGC TAC GGA CAG TAC  
193

Val Asp Pro Ala Glu Phe Phe Val Leu Thr Glu Arg Tyr Gly Gln Tyr  
255 260 265

CGG GAG ACC GTG CGC GCT CTC AGG CTA GAG TTC ACG TTG GAT GTG CGA  
241

241  
Arg Glu Thr Val Arg Ala Leu Arg Leu Glu Phe Thr Leu Asp Val Arg  
270 275 280

AGG AAA TTG CAC GAG GCC CGA GCC GGG GTT CTG GCC GAG CGC AAG GCG  
289

Arg Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala  
285                      290                      295                      300

CAG CAG GCC ATC ACG GAG CAC CGG GAG CTG ATG GCC TGG AAC CGG GAC  
337

Gln Gln Ala Ile Thr Glu His Arg Glu Leu Met Ala Trp Asn Arg Asp

305            310            315  
 GAG AAC CGG CGA ATG CAG GAG CTA CGG ATA GCG AGG TTG CAG CTG GAA  
 385  
 Glu Asn Arg Arg Met Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu  
       320            325            330  
  
 GCA CAG GCC CAG GAG GTG CAG AAG GCT GAG GCC CAG CGC CAG AGG GCT  
 433  
 Ala Gln Ala Gln Glu Val Gln Lys Ala Glu Ala Gln Arg Gln Arg Ala  
       335            340            345  
  
 CAG GAG GAG CAG GCT TGG GTG CAA CTG AAA GAG CAA GAA GTG CTC AAG  
 481  
 Gln Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys  
       350            355            360  
  
 CTG CAG GAG GAG GCA AAA AAC TTC ATC ACT CGG GAG AAC CTG GAG GCA  
 529  
 Leu Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala  
 365            370            375            380  
  
 CGG ATA GAA GAA GCG TTG GAC TCT CCG AAG AGT TAC AAC TGG GCC GTC  
 577  
 Arg Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val  
       385            390            395  
  
 ACC AAA GAA GGG CAG GTG GTC AGG AAC TGAGCACAGA GACTTCTGGG  
 624  
 Thr Lys Glu Gly Gln Val Val Arg Asn  
       400            405  
  
 GGCCCAAATA AGCACAGTGC TTGCCTAGGG TCTGTGTACT GGGATAGGAA  
 TTGGTACATC    684  
  
 CCAGGAGGAT GGCTCAGCCG TTTCCAGAGC AACCTCAGTC ACTCCAGGCT  
 CGGCACTCAC    744  
  
 CACCTGACTG GGA ACTCCCA GATGTCCCTG TTCTGGCACC ACAGTCAAAC  
 TGAGGGCAGC    804  
  
 ATTAACTCT GGGAAGTTCC TATCGCACAG AGGATCGGAC TGGACTGTGT  
 CCCTCTAGAA    864

305 310 315  
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 320 325 330  
 433  
 335 340 345  
 481  
 350 355 360  
 529  
 365 370 375 380  
 577  
 385 390 395  
 624  
 400 405  
 684  
 744  
 804  
 864

GCCAAGCTTG TCTTGTAAGT CTCTTGGAGT CCTGTGAGCC AAATGTTTCC  
TGCTTTTATA 924

AATAAAGTAT TGGAGCCCA

943

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Arg Ala Leu Asn Arg Leu Ala Gln Arg Pro Gly Asp Arg Pro  
1 5 10 15

Pro Thr Pro Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp  
20 25 30

Pro Pro Ala Lys Ser Lys Val Gly Arg Val Gln Thr Pro Pro Ala Val  
35 40 45

Asp Pro Ala Glu Phe Phe Val Leu Thr Glu Arg Tyr Gly Gln Tyr Arg  
50 55 60

Glu Thr Val Arg Ala Leu Arg Leu Glu Phe Thr Leu Asp Val Arg Arg  
65                    70                    75                    80

Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln  
85 90 95

Gln Ala Ile Thr Glu His Arg Glu Leu Met Ala Trp Asn Arg Asp Glu  
100 105 110

Asn Arg Arg Met Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala  
115 120 125

Gln Ala Gln Glu Val Gln Lys Ala Glu Ala Gln Arg Gln Arg Ala Gln  
130 135 140

Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	28	38	35	0.15	2.1	0.98	Normal
Gender	1.2	0.4	1	2	1	1	1	1	0.05	0.2	0.99	Normal
Education	12.5	2.1	9	16	12	11	13	12	0.12	1.8	0.97	Normal
Income	1500	500	500	3000	1200	800	1800	1000	0.25	3.5	0.95	Normal
Marital Status	1.8	0.6	1	3	2	1	2	2	0.08	0.3	0.99	Normal
Occupation	2.5	1.2	1	5	2	1	3	2	0.18	2.5	0.96	Normal
Health Status	1.5	0.5	1	2	1	1	1	1	0.02	0.1	0.99	Normal
Stress Level	3.2	1.5	1	5	3	2	4	3	0.10	1.5	0.98	Normal
Life Satisfaction	4.5	1.0	3	5	4	4	4	4	0.01	0.05	0.99	Normal
Work-Life Balance	2.8	1.2	1	5	3	2	4	3	0.15	2.0	0.97	Normal
Family Support	3.8	1.0	2	5	4	3	4	4	0.05	0.2	0.99	Normal
Community Involvement	2.2	1.0	1	5	2	1	3	2	0.12	1.8	0.97	Normal
Personal Growth	3.5	1.2	2	5	3	2	4	3	0.10	1.5	0.98	Normal
Overall Well-being	3.0	1.0	1	5	3	2	4	3	0.15	2.0	0.97	Normal

Lys Glu Gly Gln Val Val Arg Asn  
195 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Rat 5'OT-EST-xdel

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:1026..1270

(ix) FEATURE:

- (A) NAME/KEY: exon  
(B) LOCATION:1799..2235

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION:1030..1152

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGACCTCTGT GGATCTGATA TACATGTAAG TGACAGACCA TCCGAGCTAT  
ATAGTGAGAC 60

CTGTGCAAGG AAGGATGGAG TGCACGTTCC CTGATGTTCA GAGCAACCCT  
GTGTCCTCC 120

AGGTAGGTGA GATGAGAGGA AGAGGGTGGC CTTGGCCTGG GCCTCCTACG  
GGCCTGGAAG 180

TTGGGAGAAG GATGTAAGCA GACTCTGTTC TCTTCTGAGA AATATCAGGT  
ATTGCAGTCA 240

GCCCAGGCTC CTCAGACCCT CCTAAGTGCA GATTCTCTGC AGAATCTGGT  
GTTGACAACA 300

CTAATGAGTA GGATGAGACT TCAGTTCCCT AGCCCTCACC GTCAGCTTCT  
GATTACCAAC 360

AACTCTCCCA GAGGAGAGCC ATCTACCTTT GGGACAGATG CTCTCTGCCC  
TGCACTGCCT 420

CCTGTTTCTC TTCATTGTAG AGGAAGATAG TACTTTAAAA GCTTCATAAA  
TGGTCTCAAG 480

GTGGGAAGAC CCCGGCTCAG GTGAAAGAGG ACAAGCGTCA CCTCACACAG  
GCCACCCAGT 540

AGAAAACAAG TGATCACTGA TACTGAGAAC TCTGGCAATT GCAGAGCTGC  
CCAAGACCAC 600

AACAGGGCAG TGCAATGCAA GGAAAAGGTT TGTGCTCGA TTGCAAACCT  
AAAGTTTAAA 660

GTGCATCAGG AGAACGCTTA CTCAAAGAGG AAGTGTAAGC CTAACCTAAG  
TAGCTAGAAG 720

CTCAGAATTT CTTGCATCAG CCCTGGAAGG GTACACAGGC CACCGGTGGG  
CCAGAGAACC 780

ACACGCTTTG GGGCGGTGTC CAAGCTTGTG AACAAGTAGG CAAGAGCGCC  
TGGTGTGTA 840

CCCTGCTCAAG

AGAGTCCACC ACCCCGCACC TCCCCCGCC CCCAATCAGG TTGTCACGAT  
TCGATTCGTT 1582

AGGGTGCCCC GTTCTCCTG GGAAGGCTC CCGTCAGTG ATTTCTGTAA

CCGGACCCTG 2482

CCCTGACACA GCGTCATTGG ACTACCCAGC AGACAGTAGA CTCCACTCTA  
AACCCGCTTC 2542

TTGCGGTCAG TTGCTGTCCT TCAGTGTGTG TAAGCAGTGG CCAGACAGCA  
CCCTTGGGTG 2602

TCATTTCAAG ACTCTCTCAC CTTGGTCTGC TTTACGTTTG GTTTGATTTG  
GTTTGTTCTG 2662

GTTTTTGAGA CGAGGCCTTT CACTGGAACC TGGCACTCAG TATTTAGACT  
GCCCAGCCAG 2722

CTAGCCTCAG AGAATGCATC TCGGTATGCT TGCCTGGCGC TGGAATTCGG  
TGCACATGGC 2782

TTTGATGTGT ACCGGGGATC AGACACAGAT GTTTCATGAG TGCAGTGCAT  
GCCTGTTAGT 2842

GGTAGAGCTC 2852

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro  
1 5 10 15

Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Pro Arg Pro Arg Ser Phe  
20 25 30

Ser Ala Pro Phe Ser Ser Gln Asp Ser  
35 40

(2) INFORMATION FOR SEQ ID NO: 9:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTCACACCAC TCTGTCGAAC

20

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGAGGAAGA CAGGTGAAAG

20

## (2) INFORMATION FOR SEQ ID NO: 11:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCATGTTGCG GGCTTTGAAC

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## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TCTTTCAGTT GCACCCAAGC

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## (2) INFORMATION FOR SEQ ID NO: 13:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GTGATAGGAA CTTCCCAGAG

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(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Synthetic Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GCCTCGTGCA ATTTCCCTCG CACCTCCAAT GTGAACTCTC GC

42

(2) INFORMATION FOR SEQ ID NO: 15:

(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: YES

TCCTGCGAGG AAAAAGGAGC CGAGAATGAG CGGGGCCGTG GG

42

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(B) CLONE: Rat 5'OT-EST

(A) NAME/KEY: exon w

(B) LOCATION:1026..1241

(ix) FEATURE:

(A) NAME/KEY: exon x  
(B) LOCATION:1332..1478

(ix) FEATURE:  
(A) NAME/KEY: exon y  
(B) LOCATION:1559..1682

(ix) FEATURE:  
(A) NAME/KEY: exon z  
(B) LOCATION:2211..2647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TGACCTCTGT GGATCTGATA TACATGTAAG TGACAGACCA TCCGAGCTAT  
ATAGTGAGAC 60

CTGTGCAAGG AAGGATGGAG TGCACGTTCC CTGATGTTCA GAGCAACCCT  
GTGTCACTCC 120

AGGTAGGTGA GATGAGAGGA AGAGGGTGGC CTTGGCCTGG GCCTCCTACG  
GGCCTGGAAG 180

TTGGGAGAAG GATGTAAGCA GACTCTGTTC TCTTCTGAGA AATATCAGGT  
ATTGCAGTCA 240

GCCCAGGCTC CTCAGACCCT CCTAAGTGCA GATTCTCTGC AGAATCTGGT  
GTTGACAACA 300

CTAATGAGTA GGATGAGACT TCAGTTCCT AGCCCTCACC GTCAGCTTCT  
GATTACCAAC 360

AACTCTCCCA GAGGAGAGCC ATCTACCTTT GGGACAGATG CTCTCTGCCC  
TGCACTGCCT 420

CCTGTTTCTC TTCATTGTAG AGGAAGATAG TACTTTAAAA GCTTCATAAA  
TGGTCTCAAG 480

GTGGGAAGAC CCCGGCTCAG GTGAAAGAGG ACAAGCGTCA CCTCACACAG  
GCCACCCAGT 540

AGAAAACAAG TGATCACTGA TACTGAGAAC TCTGGCAATT GCAGAGCTGC  
CCAAGACCAC 600

TGGAACCGGG AGGAGAACCG GAGACTGCAG GAACTACGGT GCGAGAGGCG

AGAGTTATAA CTGGGCGGTC ACCAAAGAAG GGCAGGTGGT CAGGAACTGA  
GAACAGAGGC 2340

CTCTCAGGCC CAAATAAGGA CAGTGCTTGC CTAGGGACTG GATATTGGGG  
TAGAAATTGG 2400

TGCATCCCAG GAGGGTGGCA CAGCCTTGTC CAGAGCAGCC CCCATTCATT  
CTAGATTTGG 2460

CACCAGGTAT AGTACCTGTT CTGACACCAC ATACAAACTC CGGACAGCAT  
TAAACTCTGG 2520

GAAGTTCCTA TCACACAGAA GATCAGACTG GACTGTCCCC TCTAGAAGCC  
AAGAGCTGTC 2580

TCCTGAGTTT CTTGGAATAG TGTGAGCCCA ATGTTTCCTG CTTTTATAAA  
TAAACTATTG 2640

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CCCAGTTATT TGGGTCTTAA GGTTATTAGC CAAAAGCCAG TTCACCTAAC  
TGAGCCAGGA 2760

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GTAACCGGAC CCTGCCCTGA CACAGCGTCA TTGGACTACC CAGCAGACAG  
TAGACTCCAC 2940

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GTGGCCAGAC 3000

AGCACCTTG GGTGTCATT CAAGACTCTC TCACCTTGGT CTGCTTTACG  
TTTGGTTTGA 3060

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TCAGTATTTA 3120

GACTGCCCAG CCAGCTAGCC TCAGAGAATG CATCTGCGTA TGCTTGCCTG  
GCGCTGGAAT 3180

TCGGTGCACA TGGCTTTGAT GTGTACCGGG GATCAGACAC AGATGTTTCA



TGAGTGCAGT 3240

GCATGCCTGT TAGTGGTAGA GCTC

3264

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Cosmid DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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TCGTGTTGTG 120

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CAAGTGTTGC 180

TACTCTATTG CTATGAATTG TAAAATAAAT GTGTCTTCCA ATGGTCTTAG  
ATGACTCCCG 240

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ACTGATCTCC 300

AGTAACCTTC ACTTGAGTCC ATATCCTCCA TGAAGGTATG GAAGTCAATA

AAACTGAGCT 360

TCAAGCCTCA TCAAAATGGG TCCATCCCCT GGTACAGTGT GAGTGGAAGA  
ATACCCACCA 420

TACGGTCACT GGAAGGAGGA TGTCTGAAGG GTCTTAGATT GTGTCAAGGG  
GTCCTGGGTG 480

TCAGGATCTG ACGAAGCAGG CTCGTCATGT TTCATGAAGA CTACAGGTAT  
GTGATAAAAC 540

TGCAAGCTGG AAAAGTACCC ACTGAGCCCG TGTGGCTCTG CTGGGATTTG  
GAGGCATGAG 600

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AGGCTGAACT 660

GGGGTGA CTC TCTGGTGGAA AGAGTTGCCT TTAAAGAAGG AAGACATACC  
AGGCATAGCA 720

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CTGAGTTCCA 780

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CACACAAAAT 960

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GTTCACTGGT 1020

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ATGTCAGATG 1080

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ATTTTGATA 1680

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CTCGGTTGAG 1800

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GCAGTCAAGT 1980

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GCTACACCTA 2280

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TGGATTATGA CAGGACAATT TGTCCACTCA AGGTGGGCAG CTTATATCAT  
ATTAATTGGC 41400

TCTGAGTTCT TTGTCTTGGG CATTTTGTGA GCTGAGAATT TACTGATATA  
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ATAAATTACA AGCCTCTAGA GTTTTGATTT TACTGGGTTA CAGGGATTTG  
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CTGCGAGATG CTACAGCCAG AGAGACACGG ATTCTGCTAA GTAGATGACT  
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AATAGATCTT GGGGTTTCAGC ACCCAAGCTC CTCTAGTAAG CATGGGTGCA  
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TGGGAAATGC AGGCCTTCAG TGGCAGACCA AGTGGAGTCA ATGAAGTAAG  
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TCCACTTTGA CCATTCCCTG ACCCAGGTCA TAGCTGATGT GCCAGAGTGT

CATGGGTGAA 42120

GTGGTCACTT TCGCTCTTTC CACACAACCTG TGCTGTGTAA GACACCCTTT  
CTCTGGTCAT 42180

ACAGGAGTCC CCTGTGGGGT TTGAGCCCTG ACTTAAAAAG AAAGGATGAG  
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GTGGAAGGGA GCAAAGAGCA GAGGTCATTC CTGCTGGAGG AGATCTGCTA  
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GGCTACTCCA GTATGCCCTG GTCAAGACTA GCCTTGGCAA GGGAGCAGCC  
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CTAGGTGGAT AGAAGCACAC ACAGAGGATT TTCTTAGTGG TGTATGTAAT  
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ATAGAGATCC ACTTGCCTCT GCCGTCCAAG TACAGGGATT AAAGTTGCAT  
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CCCAGCCTCT CTAAAATTTT CTTAATTAAT TTATTTTTCAG AGACAGAGTC  
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GTCCTGGATA TGCTGGAACT CAGTAATGTA GAACAGGCTG TCCTTGAACA  
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CACCAACCTC TGCTTCCAAG TGCTGGGATT GAAGTGTGTG CCACTATGCC  
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CTGTTTTATT TTCTGTGCAT GGGTGTTCG CTGCATGTAT GTCTGTGCAT  
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CCGGCATCAG AGAAGGCAAG AACAGACGCA GTGTCGCACG TCTTCAATTA

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AGAGGCCAGA CTGGCCTCAG CTCAAGCCCA CAGCAGCTCC TCTGTCCTGC  
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TGTAGAGAAA TTCAGTGAGA CCAAGCTGT CTGTCCTAGG GCTATAAGCT  
GGGTGGGTGG 44520

CTGGGATGAC CACTTTGAT AGAAAAGAGG AAAAGGAACT GGGAGTTGCG  
GCCGCC 44576

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GGACAGCCCCG AAGGACTACA GGT

23

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CGAAGAACTC CGCAGGGTCC

20

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

CGAAGAACTC CGCAGGGTCC

(iv) ANTI-SENSE: NO

AAGACCCGCC ACGACCCG

18

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

GAATCAGCAC CCTCTCCGCC

20

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

TGCGGAGTTC TTCGTGCTGA TGGAG

25

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: NO

GGTGCTCGGC GGCCTCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GAGTGGCGGA GAGGGTGCTG A

21

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGCCGAGGCT GAGCGGGG

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## (2) INFORMATION FOR SEQ ID NO: 26:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CTGAAGGACG CCGCCGAGCA

20

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTCCAACGCC TGCCGCTGC

19

## (2) INFORMATION FOR SEQ ID NO: 28:

CTGAAGGACG CCGCCGAGCA

CTCCAACGCC TGCCGCTGC

(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: NO

GCAGGAGGAG CGGGAGCAGG A

21

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Synthetic Primer"

(iv) ANTI-SENSE: NO

TCCAGTGCCC CGCAAGCCG

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